

Amendments to the Claims:

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1. (Previously amended) A method of reducing pathogenicity of a fungus that produces fumonisin, comprising:
  - a) stably integrating into the genome of a plant cell a primary nucleotide sequence operably linked to a first promoter active in said plant cell, said primary nucleotide sequence comprising at least one sequence selected from the group consisting of a sequence encoding a polypeptide having fumonisin esterase activity and a sequence encoding a polypeptide having amine oxidase activity; and,
  - b) stably integrating into the genome of said plant cell a secondary nucleotide sequence operably linked to a second promoter active in said plant cell, wherein said secondary nucleotide sequence has at least 90% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10, wherein said sequence encodes a polypeptide having fumonisin detoxification activity.
2. (Original) The method of claim 1, wherein said primary nucleotide sequence encoding a polypeptide having fumonisin esterase activity is ESP1 or BEST1.
3. (Previously amended) The method of claim 1, wherein said primary nucleotide sequence encoding a polypeptide having amine oxidase activity is an amino polyamine oxidase.
4. (Original) The method of claim 1, wherein the primary nucleotide sequence stably incorporated into the plant cell comprises the sequence encoding a polypeptide having fumonisin esterase activity and the sequence encoding a polypeptide having amino oxidase activity.
5. (Original) The method of claim 1, wherein said plant is a monocot.
6. (Original) The method of claim 5, wherein said monocot is maize.

7. (Original) The method of claim 1, wherein said plant is a dicot.
8. (Previously amended) The method of claim 1, wherein at least one of said first promoter and said second promoter is an inducible promoter.
9. (Previously amended) The method of claim 8 further comprising inducing expression of said primary and said secondary nucleotide sequences for a time sufficient to reduce pathogenicity of said fungus.
10. (Previously amended) A plant having stably integrating into its genome
  - a) a primary nucleotide sequence operably linked to a promoter active in said plant, said primary nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of a sequence encoding a polypeptide having fumonisin esterase activity or a sequence encoding a polypeptide having amine oxidase activity; and,
  - b) a secondary nucleotide sequence operably linked to a promoter active in said plant, wherein said secondary nucleotide sequence has at least 90% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10, wherein said sequence encodes a polypeptide having fumonisin detoxification activity.
11. (Original) The plant of claim 10, wherein said primary nucleotide sequence encoding a polypeptide having fumonisin esterase activity is ESP1 or BEST1.
12. (Previously amended) The plant of claim 10, wherein said primary nucleotide sequence encoding a polypeptide having amine oxidase activity is an amino polyamine oxidase.
13. (Previously amended) The plant of claim 10, wherein the primary nucleotide sequence stably incorporated into the plant cell comprises a sequence encoding a polypeptide

having fumonisin esterase activity and a sequence encoding a polypeptide having amino oxidase activity.

14. (Original) The plant of claim 10, wherein said plant is a monocot.
15. (Original) The plant of claim 14, wherein said monocot is maize.
16. (Original) The plant of claim 10, wherein said plant is a dicot.
17. (Previously amended) Transformed seed of the plant of claim 10.
18. (Previously amended) A plant cell having stably integrating into its genome
  - a) a primary nucleotide sequence operably linked to a promoter active in said plant cell, said primary nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of a sequence encoding a polypeptide having fumonisin esterase activity or a sequence encoding a polypeptide having amine oxidase activity; and,
  - b) a secondary nucleotide sequence operably linked to a promoter active in said plant, wherein said secondary nucleotide sequence has at least 90% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10, wherein said sequence encodes a polypeptide having fumonisin detoxification activity.
19. (Previously amended) A method of reducing pathogenicity of a fungus that produces fumonisin, comprising stably integrating into the genome of a plant cell:
  - a) a primary nucleotide sequence operably linked to a promoter active in said plant cell, said primary nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of a sequence encoding a polypeptide having fumonisin esterase activity or a sequence encoding a polypeptide having amine oxidase activity; and,
  - b) a secondary nucleotide sequence operably linked to a promoter active in said plant cell, wherein said secondary nucleotide sequence comprises at least one sequence

selected from the group consisting of a nucleotide sequence set forth in one of SEQ ID NO: 2, 4, 7, and 10.

20. (Previously amended) A plant having stably integrating into its genome

- a) a primary nucleotide sequence operably linked to a promoter active in said plant cell, said primary nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of a sequence encoding a polypeptide having fumonisin esterase activity or a sequence encoding a polypeptide having amine oxidase activity; and,
- b) a secondary nucleotide sequence operably linked to a promoter active in said plant, wherein said secondary nucleotide sequence comprises at least one sequence selected from the group consisting of a nucleotide sequence set forth in one of SEQ ID NO: 2, 4, 7, and 10.

21. (Previously added) The method of claim 1, wherein said secondary nucleotide sequence has at least 95% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

22. (Previously added) The method of claim 1, wherein said secondary nucleotide sequence encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.

23. (Previously added) The plant of claim 10, wherein said secondary nucleotide sequence has at least 95% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

24. (Previously added) The plant of claim 10, wherein said secondary nucleotide sequence encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.

25. (Previously added) The plant of claim 10, wherein said secondary nucleotide sequence is the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

26. (Previously added) The plant cell of claim 18, wherein said secondary nucleotide sequence has at least 95% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

27. (Previously added) The plant cell of claim 18, wherein said secondary nucleotide sequence encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.

28. (Previously added) The plant cell of claim 18, wherein said secondary nucleotide sequence is the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

29. (Previously added) The method of claim 8, wherein said first promoter and said second promoter are the same promoter.

*sub E1*  
*C1*  
30. (Currently amended) The method of claim 1, wherein said primary nucleotide sequence comprises at least one sequence having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32.

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31. (Previously added) The method of claim 1, wherein said primary nucleotide sequence comprises at least one sequence having at least 90% sequence identity to the sequence set forth in SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32.

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*sub E1*  
*2*  
32. (Currently amended) The plant of claim 10, wherein said primary nucleotide sequence comprises at least one sequence having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32.

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33. (Previously added) The plant of claim 10, wherein said primary nucleotide sequence comprises at least one sequence having at least 90% sequence identity to the sequence set forth in SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, or 32.